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P#13

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/138,735

DATE: 07/05/2001
TIME: 11:22:57

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07052001\I138735.raw

ENTERED

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    3  <110> APPLICANT: PARANHOS-BACCALA, Glaucia
    4         LESENECHAL, Mylene
    5         JOLIVET, Michel
    7  <120> TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND
METHODS OF
    8         DETECTING AND TREATING CHAGAS DISEASE
   10  <130> FILE REFERENCE: WPB 36400B
   12  <140> CURRENT APPLICATION NUMBER: US 09/138,735
   13  <141> CURRENT FILING DATE: 1998-08-24
   15  <150> PRIOR APPLICATION NUMBER: US 08/480,917
   16  <151> PRIOR FILING DATE: 1995-06-07
   18  <150> PRIOR APPLICATION NUMBER: FR 94/10132
   19  <151> PRIOR FILING DATE: 1994-08-12
   21  <160> NUMBER OF SEQ ID NOS: 13
   23  <170> SOFTWARE: PatentIn version 3.0
   25  <210> SEQ ID NO: 1
   26  <211> LENGTH: 3402
   27  <212> TYPE: DNA
   28  <213> ORGANISM: Trypanosoma cruzi
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   33  gaagtacttg ccgttttgtg tgggtgacga dacaacacac atcgagcggg aagaaaaaaa   120
   35  aaaaggaaat aaattaaatt aaattatttg ttctttgaat aggcaaagaa gaagaagaag   180
   37  aaaaggtgcg ggggagggag gagaaagcga cacacacaca aaaaaaaaaa aaggaattgc   240
   39  ggaaataaca acgcaaggcg cggacatgac cgtgacggtg gatttgttca atcatgcgaa   300
   41  gccgagcaac aatgagggcc gcgtgtggtc tgtggacgcc gcgacattta acgaggtgcc   360
   43  tgaggcgcag cgtgtgctgg cggattcgca gttttatctt gcctacacca tgaagcggcg   420
   45  tcacgtgctg cgtgtggtga agcgctcgaa ccttttgaag ggcaccgtgc gggcacactc   480
   47  aaagcccatt catgcggtga agtttgtgaa ttaccgcagt^ aacgtcgcag catcggctgg   540
   49  gaaggggggag ttcttcgtgt gggttgtgac ggatgaaacg gaggcgagca acggcaagcc   600
   51  ggatctcgca gcccgcctca cagtgaaggt gtactttaag cttcaggatc ctgtcacaat   660
   53  tccatgcttt tctttcttta tcaacgccga gagtcagcgg cctgatctgc ttgtccttta   720
   55  cgaaacgcag gcggcaattc ttgacagctc ctccctcatt gagcgctttg acgtggaatc   780
   57  actggaggca acactacagc ggaattgcac aaccctgcga accctgactc aaccggttag   840
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   61  aatggtagcg gcatgcacat tacgaaaccg cagcactcca tcatgggcgt gttgcgaggg   960
   63  tgagccagtg aaggcattgc atctccttga cgcaaccgtt gaggaaaatg tcagtgttct  1020
   65  cgtggccgca tctacaaaag gggtgtacca atggctcctt acgggtgtag cagaaccaaa  1080
   67  cttgttgcgc aagtttgtca ttgatggatc tattgtcgcg atggaaagct cacgagaaac  1140
   69  gtttgccgtg tttgacgaca ggaagcagct ggcgctggtc aacatgcatt cccctcataa  1200
   71  ctttacctgc acacactaca tgatgccttg tcaggtacag cgtaacggct tttgcttcaa  1260
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   75  tctccggtcc tcccgcaggg aagaacagca gccaggccaa aaaacatcgg tagtggcgac  1380
   77  ggcgaaaccg gggtgtgtgt cctcgggcac tgacgcggcg agtagcagtc ataccaatac  1440
   79  gacttctgcc gctgctgcat ccccctgcatc accccctgtt tcagcgccag ccaaggcagc  1500
   81  cgcgcctcct gccgcggcgc gatcggctga ccgcacgtg gggagcaaga tcattgctaa  1560
   83  tctagtgaat cagctgggga ttaatgtcac ccaaaggagc gtcgtcagca ctggagcgcc  1620
   85  ggccacgacg aggtctacgg cggtgacgtc cacgactacc gccccgcagc gaacaagtcc  1680
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 87 atacgggcac aatggccgac ctgtgacggc tggattggtg gcagctaata gtggtgccag   1740
 89 cgcggcctcg tctcccacag ccgcggcgaa accaacagga gaagaaaagg cctccgcggc   1800
 91 atgtgaaacg agctccgtgg cgataaatgc gacacgcccg gcgcttcaca acgcctctct   1860
 93 cccgcaggcg ccaacggatg gcgtttttggc ggcagcagta taccagtcgg agggcgaggt   1920
 95 tcatcagtcg ctggagcggc tggagtccgt cataaccaac acgtctcggg ttctgaagtt   1980
 97 gctccctgac accattcgaa gagaccatga acaacttctg aatctgggtt tagaggcaca   2040
 99 gatgacagag ctgcagcaga gccgtccaac accgcaaaca cagccgagag acacaagctc   2100
101 cgcgaaatca tccgtgtttg agacgtacac ccttgttctc attgcggatt ccctctctcg   2160
103 caacatcacg aaggggggtga agcgtggtgt gaacgaggcc attatgttgc atctcgacca   2220
105 tgaggtgcgg cacgccatag ggaaccggct tcggcaaaca caaaagaaca tcatcaagag   2280
107 ccgcctcgat gaagcgttga aggaaagcac tacacagttt acggctcaat tgacgcaaac   2340
109 ggtggagaat ctggtgaagc gcgagcttgc cgaggtgctt ggtagcatca acggctccct   2400
111 cacttctctc gtgaaggaaa atgcctcatt acagaaagag ttgaattcca taatgtctag   2460
113 tggggtgttg gatgaaatgc gtcgtatgcg ggaagagctg tgcacattgc gagagtccgt   2520
115 tgcgaagcgg aaggcaacaa tgccagattc ttctcttcac gccacgagct cctttcaagg   2580
117 aagaaggtct gcgcccgaga caattcttgc aaccgcgtta tcgatggtgc gagagcagca   2640
119 ataccgtcag ggactggaat acatgttgat ggctcagcag ccctctctcc tcctgcggtt   2700
121 cctcagcata cttacaaggg aaaacgaaaa cgcctactcg gaacttattg aaaatgtaga   2760
123 gacgccgaat gacgtgtggt gttcggttct gttgcaactc atagaggccg cggcgaccga   2820
125 ggctgagaag gaggtggttg ttggcgtcgc cattgatatt ctctccgagc gcgatcaaat   2880
127 tgctcagaac ggcgcactcg gctcgaaact caccaccgcc atgcgagcct ttgagcgaca   2940
129 ggcaaggtcg gagacaacga gcaggtcatt cttgcaatgc ctgaagaacc tggaaaagct   3000
131 tctgcaatca tgataataaa aagaactcaa cgaatacagt tgttgattat taaggaaggg   3060
133 aaaagagaga aagagagaga gagagagaga aatgtaatgg gcgtttagtt acggtagaaa   3120
135 gaaaacgtgt ggataagaag gaggggtttt gtgtgcgacc aggaattact ggggaacgct   3180
137 gctacacggc ggaatcgacc attttattat tattattatt gtctttagta ttatgttttt   3240
139 tcttgtgtgt gtgtgtgtgt gtttgtgtgt gtgcggttat tttgtatccg tttgctcccg   3300
141 cccctgcccc ccatcacccg aggagaaagt agaataagac acatacgatt gttgtttttg   3360
143 ttatccttaa aaggaagaga gaccaaaaaa aaaaaaaaaa aa                       3402
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 915
148 <212> TYPE: PRT
149 <213> ORGANISM: Trypanosoma cruzi
151 <400> SEQUENCE: 2
153 Met Thr Val Thr Val Asp Leu Phe Asn His Ala Lys Pro Ser Asn Asn
154 1               5               10              15
156 Glu Gly Arg Val Trp Ser Val Asp Ala Ala Thr Phe Asn Glu Val Pro
157             20              25              30
159 Glu Ala Gln Arg Val Leu Ala Asp Ser Gln Phe Tyr Leu Ala Tyr Thr
160         35              40              45
162 Met Lys Arg Arg His Val Leu Arg Val Val Lys Arg Ser Asn Leu Leu
163     50              55              60
165 Lys Gly Thr Val Arg Ala His Ser Lys Pro Ile His Ala Val Lys Phe
166 65              70              75                  80
168 Val Asn Tyr Arg Ser Asn Val Ala Ala Ser Ala Gly Lys Gly Glu Phe
169             85              90              95
171 Phe Val Trp Val Val Thr Asp Glu Thr Asp Ala Ser Asn Gly Lys Pro
172             100             105                 110
174 Asp Leu Ala Ala Arg Leu Thr Val Lys Val Tyr Phe Lys Leu Gln Asp
```

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```
175          115                   120                  125
177 Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln
178     130                   135                  140
180 Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp
181 145                   150                  155                  160
183 Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr
184                   165                  170                  175
186 Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser
187              180                   185                  190
189 Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr
190          195                   200                  205
192 Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr
193     210                   215                  220
195 Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu
196 225                   230                  235                  240
198 Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser
199              245                   250                  255
201 Thr Lys Gly Val Tyr Gln Trp Leu Leu Thr Gly Val Ala Glu Pro Asn
202          260                   265                  270
204 Leu Leu Arg Lys Phe Val Ile Asp Gly Ser Ile Val Ala Met Glu Ser
205     275                   280                  285
207 Ser Arg Glu Thr Phe Ala Val Phe Asp Asp Arg Lys Gln Leu Ala Leu
208     290                   295                  300
210 Val Asn Met His Ser Pro His Asn Phe Thr Cys Thr His Tyr Met Met
211 305                   310                  315                  320
213 Pro Cys Gln Val Gln Arg Asn Gly Phe Cys Phe Asn Arg Thr Ala Asp
214              325                   330                  335
216 Gly Ser Cys Val Leu Ala Asp Met Ser Asn Arg Leu Thr Ile Phe His
217          340                   345                  350
219 Leu Arg Cys Ser Arg Arg Glu Glu Gln Gln Pro Gly Gln Lys Thr Ser
220     355                   360                  365
222 Val Val Ala Thr Ala Lys Pro Gly Cys Val Ser Ser Gly Thr Asp Ala
223     370                   375                  380
225 Ala Ser Ser Ser His Thr Asn Thr Thr Ser Ala Ala Ala Ala Ser Pro
226 385                   390                  395                  400
228 Ala Ser Pro Pro Val Ser Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala
229              405                   410                  415
231 Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn
232              420                   425                  430
234 Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser
235          435                   440                  445
237 Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr
238     450                   455                  460
240 Thr Ala Pro Gln Arg Thr Ser Pro Tyr Gly His Asn Gly Arg Pro Val
241 465                   470                  475                  480
243 Thr Ala Gly Leu Val Ala Ala Asn Ser Gly Ala Ser Ala Ala Ser Ser
244              485                   490                  495
246 Pro Thr Ala Ala Ala Lys Pro Thr Gly Glu Glu Lys Ala Ser Ala Ala
247          500                   505                  510
```

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```
249 Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His
250         515                 520                 525
252 Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala
253         530                 535                 540
255 Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu
256 545                 550                 555                 560
258 Ser Val Ile Thr Asn Thr Ser Arg Val Leu Lys Leu Leu Pro Asp Thr
259                 565                 570                 575
261 Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln
262         580                 585                 590
264 Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg
265         595                 600                 605
267 Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val
268         610                 615                 620
270 Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg
271 625                 630                 635                 640
273 Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His
274                 645                 650                 655
276 Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser
277                 660                 665                 670
279 Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln
280             675                 680                 685
282 Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val
283         690                 695                 700
285 Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala
286 705                 710                 715                 720
288 Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp
289                 725                 730                 735
291 Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val
292             740                 745                 750
294 Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser
295         755                 760                 765
297 Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala
298     770                 775                 780
300 Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met
301 785                 790                 795                 800
303 Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu
304                 805                 810                 815
306 Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu
307             820                 825                 830
309 Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala
310         835                 840                 845
312 Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp
313         850                 855                 860
315 Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser
316 865                 870                 875                 880
318 Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu
319                 885                 890                 895
321 Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu
```

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```
322                 900              905              910
324 Leu Gln Ser
325         915
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 24
329 <212> TYPE: DNA
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332 <220> FEATURE:
333 <223> OTHER INFORMATION: phage DNA primer
335 <400> SEQUENCE: 3
336 ggtggcgacg actcctggag cccg                               24
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 24
341 <212> TYPE: DNA
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C--> `342 <213> ORGANISM: Artificial`
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344 <220> FEATURE:
345 <223> OTHER INFORMATION: phage DNA primer
347 <400> SEQUENCE: 4
348 ttgacaccag accaactggt aatg                               24
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 18
353 <212> TYPE: DNA
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356 <220> FEATURE:
357 <223> OTHER INFORMATION: primer
359 <400> SEQUENCE: 5
360 tcgggcactg acgcggcg                                      18
363 <210> SEQ ID NO: 6
364 <211> LENGTH: 24
365 <212> TYPE: DNA
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C--> `366 <213> ORGANISM: Artificial`
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368 <220> FEATURE:
369 <223> OTHER INFORMATION: phage lambda gt10 DNA primer
371 <400> SEQUENCE: 6
372 cttatgagta tttcttccag ggta                               24
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
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C--> `378 <213> ORGANISM: Artificial`
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380 <220> FEATURE:
381 <223> OTHER INFORMATION: probe/primer
383 <400> SEQUENCE: 7
384 aacgctatta ttagaacagt t                                  21
387 <210> SEQ ID NO: 8
388 <211> LENGTH: 18
389 <212> TYPE: DNA
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C--> `390 <213> ORGANISM: Artificial`
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392 <220> FEATURE:
393 <223> OTHER INFORMATION: probe/primer
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VERIFICATION SUMMARY   DATE: 07/05/2001
PATENT APPLICATION: **US/09/138,735**   TIME: 11:22:58

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07052001\I138735.raw**

L:330 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:342 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:354 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:366 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
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